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Notes and Comments

New evidence of the evolutionary relationship of the *flavida* complex with the genus *Panstrongylus* (Hemiptera, Triatominae) by karyosystematic

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Scientific note

The Triatominae subfamily (Hemiptera, Reduviidae) is composed of 152 species belonging to 18 genera and five tribes (Galvão, 2014; Alevi et al., 2016; Mendonça et al., 2016; Souza et al., 2016; Rosa et al., 2017). The Triatomini tribe is the most diverse and one of the most important from the point of views epidemiological (Galvão, 2014; WHO, 2015). Schofield and Galvão (2009) grouped these triatomines in complexes and specifics subcomplexes mainly based on morphological characters and geographic disposition. The *flavida* complex consists of the species *Nesotriatoma bruneri* Usinger, 1944, *N. flavida* (Neiva, 1911) and *N. obscura* Maldonado and Farr, 1962 [although recently it has been suggested that *N. bruneri* and *N. flavida* should be again synonymized (Alevi et al., 2016)].

Recently, Justi et al. (2014, 2016) claim that although the complexes and subcomplexes show no taxonomic validity they must be monophyletic groups. Thus, the authors presented a phylogenetic reconstruction for the species groupings proposed by Schofield and Galvão (2009) and observed that many groups are not monophyletic (*brasiliensis*, *maculata*, *matogrossensis*, *flavida* and *sordida* subcomplexes). The *flavida* complex although it has formed a monophyletic group, curiously was presented as evolutionarily related to *Panstrongylus* genus, as has been observed by other authors (Hypsa et al., 2002).

Therefore, we will group all information related to the number and morphology of the chromosomes of *Nesotriatoma* spp. and *Panstrongylus* spp. with intuited of analyze the chromosomal relationship of these triatomines.

All species of *Panstrongylus* genus (except *P. megistus* and *P. lutzi*) and *Nesotriatoma* genus presents the karyotype 2n = 23 (20A + X_1X_2Y) (Table 1). Furthermore, all species of both genera (except *P. lutzi*) showed the same system of sex determination, as well as the same chromosomal characteristics (Table 1).

Recently, by means of dated phylogeny was supported that the ancestral of *Nesotriatoma* arrived in the Antillean islands approximately 14.8-18.8 millions of years (associated with rodent subfamily Capromyinae) (Justi et al., 2016) and by phylogenetic analysis we can see that *Nesotriatoma* and *Panstrongylus* share an ancestor comum (Justi et al., 2014, 2016). Was suggested that the ancestor of these vectors presented karyotype 2n = 23 and that during the divergence and karyotype evolution of species occurred one event punctual of simploidy in the autosome of *P. megistus* and agmatoploidy in the X sex chromosome of *P. lutzi* (Alevi and Azeredo-Oliveira, 2018).

Thus, by karyosystematic we confirm the phylogenetic relationship between *flavida* complex and *Panstrongylus* genus. We suggest that experimental hybrid crosses are to be conducted for analysis of possible prezygotic and postzygotic barriers installed in the *Panstrongylus* and *Nesotriatoma* genus.

Table 1. Chromosomal characteristics of the species of *flavida* complex and *Panstrongylus* genus.

Species	Chromosome number	Sex determination	Relative size of sex chromosomes	Relative size of autosomes	Reference
N. flavida	2n = 23	X_1X_2Y	Y>Xs	Small variation	Dujardin et al. (2002)
N. bruneri	2n = 23	X_1X_2Y	Y>Xs	Small variation	Alevi et al. (2016)
N. obscura	-	-	-		
P. chinai	2n = 23	X_1X_2Y	Y>Xs	Small variation	Pérez et al. (2002)
P. diasi	-	-	-		
P. geniculatus	2n = 23	X_1X_2Y	Y>Xs	Small variation	Pérez et al. (2002)
P. guentheri	-	-	-		
P. hispaniolae	-	-	-		
P. howardi	2n = 23	X_1X_2Y	Y>Xs	Small variation	Dujardin et al. (2002)
P. humeralis	-	-	-		
P. lenti	-	-	-		
P. lutzi	2n = 24	$X_1X_2X_3Y$	Y>Xs	Small variation	Santos et al. (2016), Alevi et al. (2017)
P. lignarius	2n = 23	X_1X_2Y	Y>Xs	Small variation	Pérez et al. (2002)
P. megistus	2n = 21	X_1X_2Y	Y>Xs	Small variation	Schreiber and Pellegrino (1950)
P. mitarakaensis	-	-	-		
P. rufotuberculatus	2n = 23	X_1X_2Y	Y>Xs	Small variation	Pérez et al. (2002)
P. tupynambai	2n = 23	X_1X_2Y	Y>Xs	Small variation	Pérez et al. (2002)

X: X sex chromosome; Y: Y sex chromosome.

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